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RAW SEQUENCE LISTING DATE: 03/27/2002
PATENT APPLICATION: **US/10/092,640** TIME: 14:24:25

Input Set : **A:\407T-897221US seq list.txt**
Output Set: **N:\CRF3\03272002\J092640.raw**

SEQUENCE LISTING

```
 4 (1) GENERAL INFORMATION:
 6      (i) APPLICANT: Marks, James D.
 7                    Schier, Robert
 9     (ii) TITLE OF INVENTION: Novel High Affinity Human Antibodies to
10                             Tumor Antigens
12    (iii) NUMBER OF SEQUENCES: 141
14     (iv) CORRESPONDENCE ADDRESS:
15           (A) ADDRESSEE: Quine Intellectual Property Law Group P.C.
16           (B) STREET: 2033 Clement Ave. Suite 200
17           (C) CITY: Alameda
18           (D) STATE: California
19           (E) COUNTRY: USA
20           (F) ZIP: 94501
22      (v) COMPUTER READABLE FORM:
23           (A) MEDIUM TYPE: Floppy disk
24           (B) COMPUTER: IBM PC compatible
25           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28     (vi) CURRENT APPLICATION DATA:
C--> 29      (A) APPLICATION NUMBER: US/10/092,640
C--> 30      (B) FILING DATE: 05-Mar-2002
31           (C) CLASSIFICATION:
45    (vii) PRIOR APPLICATION DATA:
34           (A) APPLICATION NUMBER: US 60/000,238
35           (B) FILING DATE: 14-JUN-1995
38           (A) APPLICATION NUMBER: US 60/000,250
39           (B) FILING DATE: 15-JUN-1995
42           (A) APPLICATION NUMBER: US 08/665,202
43           (B) FILING DATE: 13-JUN-1996
46           (A) APPLICATION NUMBER: US 09/315,574
47           (B) FILING DATE: 20-MAY-1999
49   (viii) ATTORNEY/AGENT INFORMATION:
50           (A) NAME: Hunter, Tom
51           (B) REGISTRATION NUMBER: 38,498
52           (C) REFERENCE/DOCKET NUMBER: 02307E-061411
54     (ix) TELECOMMUNICATION INFORMATION:
55           (A) TELEPHONE: (415) 576-0200
56           (B) TELEFAX: (415) 576-0300
59 (2) INFORMATION FOR SEQ ID NO: 1:
61      (i) SEQUENCE CHARACTERISTICS:
62           (A) LENGTH: 15 amino acids
63           (B) TYPE: amino acid
```

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```
     (C) STRANDEDNESS:
     (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1               5                  10                  15
(2) INFORMATION FOR SEQ ID NO: 2:
 (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 5 amino acids
     (B) TYPE: amino acid
     (C) STRANDEDNESS:
     (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 Ser Ser Ser Ser Gly
 1               5
(2) INFORMATION FOR SEQ ID NO: 3:
 (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 15 amino acids
     (B) TYPE: amino acid
     (C) STRANDEDNESS:
     (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly
 1               5                  10                  15
(2) INFORMATION FOR SEQ ID NO: 4:
 (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 774 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear
W--> (ii) MOLECULE TYPE: DNA
(ix) FEATURE:
     (A) NAME/KEY: CDS
     (B) LOCATION: 1..774
     (D) OTHER INFORMATION: /note= "sequence of C6 sFv
antibody C6.5"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
CAG GTG CAG CTG TTG CAG TCT GGG GCA GAG TTG AAA AAA CCC GGG GAG        48
Gln Val Gln Leu Leu Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Glu
  1               5                  10                  15
TCT CTG AAG ATC TCC TGT AAG GGT TCT GGA TAC AGC TTT ACC AGC TAC        96
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
             20                  25                  30
TGG ATC GCC TGG GTG CGC CAG ATG CCC GGG AAA GGC CTG GAG TAC ATG       144
Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
          35                  40                  45
GGG CTC ATC TAT CCT GGT GAC TCT GAC ACC AAA TAC AGC CCG TCC TTC       192
```

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```
143 Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
144      50                  55                  60
146 CAA GGC CAG GTC ACC ATC TCA GTC GAC AAG TCC GTC AGC ACT GCC TAC       240
147 Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
148  65                  70                  75                  80
150 TTG CAA TGG AGC AGT CTG AAG CCC TCG GAC AGC GCC GTG TAT TTT TGT       288
151 Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
152                 85                  90                  95
154 GCG AGA CAT GAC GTG GGA TAT TGC AGT AGT TCC AAC TGC GCA AAG TGG       336
155 Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp
156             100                 105                 110
158 CCT GAA TAC TTC CAG CAT TGG GGC CAG GGC ACC CTG GTC ACC GTC TCC       384
159 Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
160         115                 120                 125
162 TCA GGT GGA GGC GGT TCA GGC GGA GGT GGC TCT GGC GGT GGC GGA TCG       432
163 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
164     130                 135                 140
166 CAG TCT GTG TTG ACG CAG CCG CCC TCA GTG TCT GCG GCC CCA GGA CAG       480
167 Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
168 145                 150                 155                 160
170 AAG GTC ACC ATC TCC TGC TCT GGA AGC AGC TCC AAC ATT GGG AAT AAT       528
171 Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
172                 165                 170                 175
174 TAT GTA TCC TGG TAC CAG CAG CTC CCA GGA ACA GCC CCC AAA CTC CTC       576
175 Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
176             180                 185                 190
178 ATC TAT GGT CAC ACC AAT CGG CCC GCA GGG GTC CCT GAC CGA TTC TCT       624
179 Ile Tyr Gly His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser
180         195                 200                 205
182 GGC TCC AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC AGT GGG TTC CGG       672
183 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg
184     210                 215                 220
186 TCC GAG GAT GAG GCT GAT TAT TAC TGT GCA GCA TGG GAT GAC AGC CTG       720
187 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
188 225                 230                 235                 240
190 AGT GGT TGG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT GCG       768
191 Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala
192                 245                 250                 255
194 GCC GCA                                                           774
195 Ala Ala
198 (2) INFORMATION FOR SEQ ID NO: 5:
200      (i) SEQUENCE CHARACTERISTICS:
201           (A) LENGTH: 258 amino acids
202           (B) TYPE: amino acid
203           (D) TOPOLOGY: linear
205      (ii) MOLECULE TYPE: protein
207      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
209 Gln Val Gln Leu Leu Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Glu
210   1               5                  10                  15
```

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```
212 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
213              20                  25                  30
215 Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
216          35                  40                  45
218 Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
219      50                  55                  60
221 Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
222  65                  70                  75                  80
224 Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
225                  85                  90                  95
227 Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp
228              100                 105                 110
230 Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
231          115                 120                 125
233 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
234      130                 135                 140
236 Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
237 145                 150                 155                 160
239 Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
240                 165                 170                 175
242 Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
243              180                 185                 190
245 Ile Tyr Gly His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser
246          195                 200                 205
248 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg
249      210                 215                 220
251 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
252 225                 230                 235                 240
254 Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala
255                 245                 250                 255
257 Ala Ala
260 (2) INFORMATION FOR SEQ ID NO: 6:
262      (i) SEQUENCE CHARACTERISTICS:
263           (A) LENGTH: 11 amino acids
264           (B) TYPE: amino acid
265           (C) STRANDEDNESS:
266           (D) TOPOLOGY: linear
268     (ii) MOLECULE TYPE: peptide
271     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
273      Ala Ala Trp Asp Asp Ser Leu Ser Gly Trp Val
274      1               5                   10
277 (2) INFORMATION FOR SEQ ID NO: 7:
279      (i) SEQUENCE CHARACTERISTICS:
280           (A) LENGTH: 11 amino acids
281           (B) TYPE: amino acid
282           (C) STRANDEDNESS:
283           (D) TOPOLOGY: linear
285     (ii) MOLECULE TYPE: peptide
288     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
```

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Input Set : A:\407T-897221US seq list.txt
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```
290      Ala Ala Trp Asp Tyr Ser Leu Ser Gly Trp Val
291      1               5                   10
294 (2) INFORMATION FOR SEQ ID NO: 8:
296      (i) SEQUENCE CHARACTERISTICS:
297           (A) LENGTH: 11 amino acids
298           (B) TYPE: amino acid
299           (C) STRANDEDNESS:
300           (D) TOPOLOGY: linear
302     (ii) MOLECULE TYPE: peptide
305     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
307      Ala Ala Trp Asp His Ser Leu Ser Gly Trp Val
308      1               5                   10
311 (2) INFORMATION FOR SEQ ID NO: 9:
313      (i) SEQUENCE CHARACTERISTICS:
314           (A) LENGTH: 11 amino acids
315           (B) TYPE: amino acid
316           (C) STRANDEDNESS:
317           (D) TOPOLOGY: linear
319     (ii) MOLECULE TYPE: peptide
322     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
324      Ala Ser Trp Asp Tyr Ser Leu Ser Gly Trp Val
325      1               5                   10
328 (2) INFORMATION FOR SEQ ID NO: 10:
330      (i) SEQUENCE CHARACTERISTICS:
331           (A) LENGTH: 11 amino acids
332           (B) TYPE: amino acid
333           (C) STRANDEDNESS:
334           (D) TOPOLOGY: linear
336     (ii) MOLECULE TYPE: peptide
339     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
341      Ala Ala Trp Asp Tyr Ser Leu Trp Gly Trp Val
342      1               5                   10
345 (2) INFORMATION FOR SEQ ID NO: 11:
347      (i) SEQUENCE CHARACTERISTICS:
348           (A) LENGTH: 11 amino acids
349           (B) TYPE: amino acid
350           (C) STRANDEDNESS:
351           (D) TOPOLOGY: linear
353     (ii) MOLECULE TYPE: peptide
356     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
358      Ala Thr Trp Asp Tyr Ala Leu Ser Gly Trp Val
359      1               5                   10
362 (2) INFORMATION FOR SEQ ID NO: 12:
364      (i) SEQUENCE CHARACTERISTICS:
365           (A) LENGTH: 11 amino acids
366           (B) TYPE: amino acid
367           (C) STRANDEDNESS:
368           (D) TOPOLOGY: linear
370     (ii) MOLECULE TYPE: peptide
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VERIFICATION SUMMARY DATE: 03/27/2002
PATENT APPLICATION: US/10/092,640 TIME: 14:24:26

Input Set : A:\407T-897221US seq list.txt
Output Set: N:\CRF3\03272002\J092640.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:118 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:1719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:32
L:2021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72 after pos.:0
L:2734 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=110
L:2750 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=111
L:2766 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=112
L:2782 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=113
L:2798 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=114
L:2814 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=115
L:2830 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=116
L:2846 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=117
L:2862 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=118
L:2878 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=119
L:2894 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=120
L:2910 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=121
L:2926 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=122
L:2942 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=123
L:2958 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=124
L:2976 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=125
L:2994 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=126
L:3010 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=127
L:3026 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=128
L:3042 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=129
L:3058 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=130
L:3074 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=131
L:3090 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=132
L:3106 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=133
L:3122 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=134
L:3140 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=135
L:3158 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=136
L:3176 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=137
L:3192 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=138
L:3208 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=139
L:3224 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=140
L:3240 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=141